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RAW SEQUENCE LISTING

DATE: 02/15/2002

PATENT APPLICATION: US/09/882,735

TIME: 14:01:07

Input Set : A:\02006seq.txt

Output Set: N:\CRF3\02152002\I882735.raw

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3 <110> APPLICANT: Fisher F., Eric
4     Edwards K., Carl
5     Kieft L., Gary
7 <120> TITLE OF INVENTION: Truncated Soluble Tumor Necrosis Factor Type-I and
8     Type-II Receptors
10 <130> FILE REFERENCE: 02-006
12 <140> CURRENT APPLICATION NUMBER: 09/882,735
13 <141> CURRENT FILING DATE: 2001-06-15
15 <150> PRIOR APPLICATION NUMBER: 09/214,613
16 <151> PRIOR FILING DATE: 1999-01-08
18 <150> PRIOR APPLICATION NUMBER: PCT/US97/12244
19 <151> PRIOR FILING DATE: 1997-07-09
21 <150> PRIOR APPLICATION NUMBER: 60/039,792
22 <151> PRIOR FILING DATE: 1997-03-04
24 <150> PRIOR APPLICATION NUMBER: 60/039,314
25 <151> PRIOR FILING DATE: 1997-02-07
27 <150> PRIOR APPLICATION NUMBER: 60/037,737
28 <151> PRIOR FILING DATE: 1997-01-23
30 <150> PRIOR APPLICATION NUMBER: 60/032,354
31 <151> PRIOR FILING DATE: 1996-12-06
33 <150> PRIOR APPLICATION NUMBER: 60/021,443
34 <151> PRIOR FILING DATE: 1996-07-09
36 <160> NUMBER OF SEQ ID NOS: 30
38 <170> SOFTWARE: PatentIn Ver. 2.0
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42 <212> TYPE: DNA
43 <213> ORGANISM: Homo sapiens
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46 <221> NAME/KEY: CDS
47 <222> LOCATION: (1)..(483)
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51 Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser
52   1             5             10             15
54 att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat gac tgt      96
55 Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys
56             20             25             30
58 cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc tcc      144
59 Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser
60             35             40             45
62 ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc aaa      192
63 Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys

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64      50      55      60
66 tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg gac 240
67 Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
68 65      70      75      80
70 cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat tat tgg 288
71 Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp
72      85      90      95
74 agt gaa aac ctt ttc cag tgc ttc aat tgc agc ctc tgc ctc aat ggg 336
75 Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly
76      100      105      110
78 acc gtg cac ctc tcc tgc cag gag aaa cag aac acc gtg tgc acc tgc 384
79 Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys
80      115      120      125
82 cat gca ggt ttc ttt cta aga gaa aac gag tgt gtc tcc tgt agt aac 432
83 His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn
84      130      135      140
86 tgt aag aaa agc ctg gag tgc acg aag ttg tgc cta ccc cag att gag 480
87 Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu
88 145      150      155      160
90 aat 483
91 Asn
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95 <211> LENGTH: 161
96 <212> TYPE: PRT
97 <213> ORGANISM: Homo sapiens
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101 1      5      10      15
103 Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys
104      20      25      30
106 Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser
107      35      40      45
109 Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys
110      50      55      60
112 Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
113 65      70      75      80
115 Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp
116      85      90      95
118 Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly
119      100      105      110
121 Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys
122      115      120      125
124 His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn
125      130      135      140
127 Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu
128 145      150      155      160
130 Asn
134 <210> SEQ ID NO: 3
135 <211> LENGTH: 332

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136 <212> TYPE: DNA
137 <213> ORGANISM: Artificial Sequence
139 <220> FEATURE:
140 <223> OTHER INFORMATION: Description of Artificial Sequence: sTNFR-I
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143 <220> FEATURE:
144 <221> NAME/KEY: CDS
145 <222> LOCATION: (4)..(321)
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150     1           5           10           15
152 aat tcg att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat    96
153 Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn
154     20           25           30
156 gac tgt cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc    144
157 Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser
158     35           40           45
160 ggc tcc ttc acc gct tca gaa aac cac ctg aga cac tgc ctg agc tgc    192
161 Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys
162     50           55           60
164 tcc aaa tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca    240
165 Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr
166     65           70           75
168 gtg gac cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat    288
169 Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His
170     80           85           90           95
172 tat tgg agt gaa aac ctt ttc cag tgc ttc tgc tgataggatc c        332
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174     100           105
177 <210> SEQ ID NO: 4
178 <211> LENGTH: 106
179 <212> TYPE: PRT
180 <213> ORGANISM: Artificial Sequence
182 <220> FEATURE:
183 <223> OTHER INFORMATION: Description of Artificial Sequence: sTNFR-I
184     2.6D/C105
186 <400> SEQUENCE: 4
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188     1           5           10           15
190 Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp
191     20           25           30
193 Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly
194     35           40           45
196 Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser
197     50           55           60
199 Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val
200     65           70           75           80
202 Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr

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206                100                105
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212 <213> ORGANISM: Artificial Sequence
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218 <220> FEATURE:
219 <221> NAME/KEY: CDS
220 <222> LOCATION: (4)..(330)
222 <400> SEQUENCE: 5
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224      Met Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn
225      1                5                10                15
227 aat tcg att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat      96
228 Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn
229      20                25                30
231 gac tgt cca gcc ccg ggg cag gat acg gac tgc agg gag tgt gag agc      144
232 Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser
233      35                40                45
235 gcc tcc ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc      192
236 Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys
237      50                55                60
239 tcc aaa tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca      240
240 Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr
241      65                70                75
243 gtg gac cgg gac acc gtg tgt gcc tgc agg aag aac cag tac cgg cat      288
244 Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His
245      80                85                90                95
247 tat tgg agt gaa aac ctt ttc cag tgc ttc aat tgc tct ctg taaaagctt 339
248 Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu
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253 <211> LENGTH: 109
254 <212> TYPE: PRT
255 <213> ORGANISM: Artificial Sequence
257 <220> FEATURE:
258 <223> OTHER INFORMATION: Description of Artificial Sequence: sTNFR-I
259      2.6D/C106
261 <400> SEQUENCE: 6
262 Met Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn
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265 Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp
266      20                25                30
268 Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly
269      35                40                45

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271 Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser
272      50                      55                      60
274 Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val
275 65                      70                      75                      80
277 Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr
278                      85                      90                      95
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281      100                      105
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287 <213> ORGANISM: Artificial Sequence
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291      2.6D/N105
293 <220> FEATURE:
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295 <222> LOCATION: (4)..(321)
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298 cat atg gac agc gtt tgc ccc caa gga aaa tat atc cac cct caa aat      48
299      Met Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn
300      1                      5                      10                      15
302 aat tgc att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat      96
303 Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn
304                      20                      25                      30
306 gac tgt cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc      144
307 Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser
308                      35                      40                      45
310 ggc tcc ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc      192
311 Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys
312      50                      55                      60
314 tcc aaa tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca      240
315 Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr
316      65                      70                      75
318 gtg gac cgg gac acc gtg tgt ggt tgc agg aag aac cag tac cgg cat      288
319 Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His
320      80                      85                      90                      95
322 tat tgg agt gaa aac ctt ttc cag tgc ttc aat taatagggat cc      333
323 Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn
324      100                      105
327 <210> SEQ ID NO: 8
328 <211> LENGTH: 106
329 <212> TYPE: PRT
330 <213> ORGANISM: Artificial Sequence
332 <220> FEATURE:
333 <223> OTHER INFORMATION: Description of Artificial Sequence: sTNFR-I
334      2.6D/N105
336 <400> SEQUENCE: 8
337 Met Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/882,735

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